

cells with PE-labeled goat anti-human Ig to detect chimeric SDF-Fc polypeptide remaining after the 3- or 15-hour incubation (data not shown).

Down-regulation of receptor by binding of MIP-1 $\alpha$ -Fc and MIP-1 $\beta$ -Fc chimeric polypeptides to cells is determined by an assay for receptor down-regulation analogous to that described above.

## SEQUENCE LISTING

- 10 (1) GENERAL INFORMATION:
- (i) APPLICANT: Herrmann, Steve  
Swanberg, Stephen
- 15 (ii) TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
CHEMOKINE DOMAINS
- (iii) NUMBER OF SEQUENCES: 10
- 20 (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Genetics Insititute, Inc.  
(B) STREET: 87 CambridgePark  
(C) CITY: Cambridge  
(D) STATE: MA  
25 (E) COUNTRY: USA  
(F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
- 30 (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- 35 (A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- 40 (A) NAME: Sprunger, Suzanne  
(B) REGISTRATION NUMBER: P-41,323  
(C) REFERENCE/DOCKET NUMBER: GI5291
- (ix) TELECOMMUNICATION INFORMATION:
- 45 (A) TELEPHONE: (617) 498-8284  
(B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

1	Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala	Leu
					5				10						15	
15	Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys
			20						25					30		
	Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys
			35					40					45			
20	Ile	Leu	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys
	50					55						60				
	Asn	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln
25	65				70						75					80
	Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Gly	Ser	Gly
				85						90					95	
30	Ser	Gly	Ser	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala
			100						105					110		
	Pro	Glu	Phe	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			115					120					125			
35	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
	130						135					140				
	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
40	145				150						155					160
	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
				165						170					175	
45	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
			180						185					190		
	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
			195				200						205			
50	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
	210						215					220				
	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
55	225				230						235					240
	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
				245						250					255	
60	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
			260						265					270		
	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr

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ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACA CAGAAGAGCC TCTCCCTGTC 1200  
TCTGGGTAAA TGATAAGAAT TC 1222

5 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 326 amino acids  
(B) TYPE: amino acid  
10 (C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala	Leu
	1				5					10					15	
	Cys	Leu	Ser	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys	Arg	Phe
				20					25					30		
25	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu
				35				40					45			
	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn
30		50					55					60				
	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr
	65					70					75					80
35	Leu	Glu	Lys	Ala	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly
					85					90					95	
	Ser	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	Glu
				100					105					110		
40	Phe	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
			115					120					125			
	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
45		130					135					140				
	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly
	145					150					155					160
50	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn
					165					170					175	
	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
				180					185					190		
55	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro
			195					200					205			
	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu
60		210					215					220				
	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn
	225					230					235					240

5           Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
                                   245                                   250                                   255  
           Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
                                   260                                   265                                   270  
           Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg  
                                   275                                   280                                   285  
 10        Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys  
                                   290                                   295                                   300  
           Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
                                   305                                   310                                   315                                   320  
 15        Ser Leu Ser Leu Gly Lys  
                                   325

## (2) INFORMATION FOR SEQ ID NO:4:

20           (i) SEQUENCE CHARACTERISTICS:  
                   (A) LENGTH: 1216 base pairs  
                   (B) TYPE: nucleic acid  
                   (C) STRANDEDNESS: double  
 25           (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35           GCGGCCGCGC CATGAACGCC AAGGTCGTGG TCGTGCTGGT CCTCGTGCTG ACCGCGCTCT           60  
           GCCTCAGCAA GCCCGTCAGC CTGAGCTACA GATGCCCATG CCGATTCTTC GAAAGCCATG           120  
           TTGCCAGAGC CAACGTCAAG CATCTCAAAA TTCTCAACAC TCCAAACTGT GCCCTTCAGA           180  
 40           TTGTAGCCCG GCTGAAGAAC AACAAACAGAC AAGTGTGCAT TGACCCGAAG CTAAAGTGGA           240  
           TTCAGGAGTA CCTGGAGAAA GCTTTAAACA AGGGATCCGG CTCTGGGAGC GGCTCTGGCT           300  
           CTGAGTCCAA ATATGGTCCC CCATGCCCAT CATGTCCAGG TAAGCCAACC CAGGCCTCGC           360  
 45           CCTCCAGCTC AAGGCGGGAC AGGTGCCCTA GAGTAGCCTG CATCCAGGGA CAGGCCCCAG           420  
           CCGGGTGCTG ACGCATCCAC CTCCATCTCT TCCTCAGCAC CTGAGTTCGA GGGGGCACCA           480  
 50           TCAGTCTTCC TGTTCCCCCC AAAACCCAAG GACACTCTCA TGATCTCCCG GACCCCTGAG           540  
           GTCACGTGCG TGGTGGTGGA CGTGAGCCAG GAAGACCCCG AGGTCCAGTT CAACTGGTAC           600  
           GTGGATGGCG TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTTCAACAGC           660  
 55           ACGTACCGTG TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA CGGCAAGGAG           720  
           TACAAGTGCA AGGTCTCCAA CAAAGGCCTC CCGTCCTCCA TCGAGAAAAC CATCTCCAAA           780  
 60           GCCAAAGGTG GGACCCACGG GGTGCGAGGG CCACACGGAC AGAGGTCAGC TCGGCCCCACC           840  
           CTCTGCCCTG GGAGTGACCG CTGTGCCAAC CTCTGTCCCT ACAGGGCAGC CCCGAGAGCC           900

ACAGGTGTAC ACCCTGCCCC CATCCCAGGA GGAGATGACC AAGAACCAGG TCAGCCTGAC 960  
 CTGCCTGGTC AAAGGCTTCT ACCCCAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA 1020  
 5 GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT 1080  
 CTACAGCAGG CTAACCGTGG ACAAGAGCAG GTGGCAGGAG GGAATGTCT TCTCATGCTC 1140  
 10 CGTGATGCAT GAGGCTCTGC ACAACCACTA CACACAGAAG AGCCTCTCCC TGTCTCTGGG 1200  
 TAAATGATAA GAATTC 1216

## (2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala  
 1 5 10 15  
 30 Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala  
 20 25 30  
 35 Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala  
 35 40 45  
 Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe  
 50 55 60  
 40 Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp  
 65 70 75 80  
 Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Gly Ser Gly Ser  
 85 90 95  
 45 Gly Ser Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser  
 100 105 110  
 50 Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro  
 115 120 125  
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
 130 135 140  
 55 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn  
 145 150 155 160  
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
 165 170 175  
 60 Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
 180 185 190

	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
			195					200					205			
5	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
		210					215					220				
	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
	225					230					235					240
10	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
					245					250					255	
	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
15				260					265					270		
	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
			275					280					285			
20	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly
	290						295					300				
	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	305					310					315					320
25	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys					
					325					330						

## (2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	GCGGCCGCCC AATCATGCAG GTCTCCACTG CTGCCCTTGC TGTCTCCTC TGCACCATGG	60
45	CTCTCTGCAA CCAGTTCTCT GCATCACTTG CTGCTGACAC GCCGACCGCC TGCTGCTTCA	120
	GCTACACCTC CCGGCAGATT CCACAGAATT TCATAGCTGA CTACTTTGAG ACGAGCAGCC	180
50	AGTGCTCCAA GCCCGGTGTC ATCTTCCTAA CCAAGCGAAG CCGGCAGGTC TGTGCTGACC	240
	CCAGTGAGGA GTGGGTCCAG AAATACGTCA GTGACCTGGA GCTGAGTGCC GGATCCGGCT	300
	CTGGGAGCGG CTCTGGCTCT GAGTCCAAAT ATGGTCCCCC ATGCCCATCA TGTCCAGGTA	360
55	AGCCAACCCA GGCCTCGCCC TCCAGCTCAA GGCGGGACAG GTGCCCTAGA GTAGCCTGCA	420
	TCCAGGGACA GGCCCCAGCC GGGTGCTGAC GCATCCACCT CCATCTCTTC CTCAGCACCT	480
60	GAGTTCGAGG GGGCACCATC AGTCTTCCTG TTCCCCCAA AACCCAAGGA CACTCTCATG	540
	ATCTCCCGGA CCCCTGAGGT CACGTGCGTG GTGGTGGACG TGAGCCAGGA AGACCCCGAG	600
	GTCCAGTTCA ACTGGTACGT GGATGGCGTG GAGGTGCATA ATGCCAAGAC AAAGCCGCGG	660

5 GAGGAGCAGT TCAACAGCAC GTACCGTGTG GTCAGCGTCC TCACCGTCCT GCACCAGGAC 720  
 TGGCTGAACG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA AAGGCCTCCC GTCCTCCATC 780  
 10 GAGAAAACCA TCTCCAAAGC CAAAGGTGGG ACCCACGGGG TGCAGGGGCC ACACGGACAG 840  
 AGGTCAGCTC GGCCACCCCT CTGCCCTGGG AGTGACCGCT GTGCCAACCT CTGTCCCTAC 900  
 AGGGCAGCCC CGAGAGCCAC AGGTGTACAC CCTGCCCCCA TCCCAGGAGG AGATGACCAA 960  
 15 GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAC CCCAGCGACA TCGCCGTGGA 1020  
 GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC 1080  
 CGACGGCTCC TTCTTCCTCT ACAGCAGGCT AACCGTGGAC AAGAGCAGGT GGCAGGAGGG 1140  
 GAATGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA CACAGAAGAG 1200  
 20 CCTCTCCCTG TCTCTGGGTA AATGATAAGA ATTC 1234

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 331 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35 Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala  
 1 5 10 15  
 40 Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr  
 20 25 30  
 Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val  
 35 40 45  
 45 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val  
 50 55 60  
 Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser  
 65 70 75 80  
 50 Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn Gly Ser Gly Ser  
 85 90 95  
 Gly Ser Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser  
 55 100 105 110  
 Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro  
 115 120 125  
 60 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
 130 135 140  
 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn



	145		150		155		160									
	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
					165					170					175	
5	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
				180					185					190		
	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
10			195					200					205			
	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
		210					215					220				
15	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
	225					230					235					240
	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
20					245					250					255	
	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
				260					265					270		
	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
25			275					280					285			
	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly
		290					295					300				
30	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	305					310					315					320
	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys					
35					325					330						

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 1235 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50	GCGGCCGCCA ATACCATGAA GCTCTGCGTG ACTGTCCTGT CTCTCCTCAT GCTAGTAGCT	60
	GCCTTCTGCT CTCCAGCGCT CTCAGACCA ATGGGCTCAG ACCCTCCAC CGCCTGCTGC	120
55	TTTTCTTACA CCGCGAGGAA GCTTCCTCGC AACTTTGTGG TAGATTACTA TGAGACCAGC	180
	AGCCTCTGCT CCCAGCCAGC TGTGGTATTC CAAACCAAAA GAAGCAAGCA AGTCTGTGCT	240
	GATCCCAGTG AATCCTGGGT CCAGGAGTAC GTGTATGACC TGGAAGTCAA CGGATCCGGC	300
60	TCTGGGAGCG GCTCTGGCTC TGAGTCCAAA TATGGTCCCC CATGCCCATC ATGTCCAGGT	360
	AAGCCAACCC AGGCCTCGCC CTCCAGCTCA AGGCGGGACA GGTGCCCTAG AGTAGCCTGC	420

ATCCAGGGAC AGGCCCCAGC CGGGTGCTGA CGCATCCACC TCCATCTCTT CCTCAGCACC 480  
 TGAGTTCGAG GGGGCACCAT CAGTCTTCCT GTTCCCCCA AAACCCAAGG ACACTCTCAT 540  
 5 GATCTCCCGG ACCCCTGAGG TCACGTGCGT GGTGGTGGAC GTGAGCCAGG AAGACCCCGA 600  
 GGTCCAGTTC AACTGGTACG TGGATGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG 660  
 10 GGAGGAGCAG TTCAACAGCA CGTACCGTGT GGTCAGCGTC CTCACCGTCC TGCACCAGGA 720  
 CTGGCTGAAC GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC AAAGGCCTCC CGTCCTCCAT 780  
 CGAGAAAACC ATCTCCAAAG CCAAAGGTGG GACCCACGGG GTGCGAGGGC CACACGGACA 840  
 15 GAGGTCAGCT CGGCCACCC TCTGCCCTGG GAGTGACCGC TGTGCCAACC TCTGTCCCTA 900  
 CAGGGCAGCC CCGAGAGCCA CAGGTGTACA CCCTGCCCCC ATCCCAGGAG GAGATGACCA 960  
 AGAACCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA CCCCAGCGAC ATCGCCGTGG 1020  
 20 AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC GTGCTGGACT 1080  
 CCGACGGCTC CTTCTTCCTC TACAGCAGGC TAACCGTGGA CAAGAGCAGG TGGCAGGAGG 1140  
 25 GGAATGTCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC ACACAGAAGA 1200  
 GCCTCTCCCT GTCTCTGGGT AAATGATAAG AATTC 1235

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45	Met	Gln	Val	Ser	Thr	Ala	Ala	Leu	Ala	Val	Leu	Leu	Cys	Thr	Met	Ala
	1				5					10					15	
	Leu	Cys	Asn	Gln	Phe	Ser	Ala	Ser	Leu	Ala	Ala	Asp	Thr	Pro	Thr	Ala
			20						25					30		
50	Cys	Cys	Phe	Ser	Tyr	Thr	Ser	Arg	Gln	Ile	Pro	Gln	Asn	Phe	Ile	Ala
			35					40					45			
	Asp	Tyr	Phe	Glu	Thr	Ser	Ser	Gln	Cys	Ser	Lys	Pro	Gly	Val	Ile	Phe
55		50					55					60				
	Leu	Thr	Lys	Arg	Ser	Arg	Gln	Val	Cys	Ala	Asp	Pro	Ser	Glu	Glu	Trp
	65				70					75					80	
60	Val	Gln	Lys	Tyr	Val	Ser	Asp	Leu	Glu	Leu	Ser	Ala				
				85						90						

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 92 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15	Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala	1 5 10 15
	Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr	20 25 30
20	Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val	35 40 45
	Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val	50 55 60
25	Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser	65 70 75 80
30	Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn	85 90